Amendments to the Specification

Additions are indicated by underlining and deletions are indicated by ~~strikethrough~~. Only this marked-up version of the amendment is provided, in accordance with the revised amendment format as set forth in 1267 OG 106 (February 25, 2003), in which the requirement for an unmarked version is waived.

Please delete the paragraph beginning at page 35, line 28, with the following rewritten paragraph:

Optionally, a second population of staggered, non-redundant oligonucleotides can be synthesized which fill in the space left open due to the termination of the oligo at the redundant codon. This population is generated in an analogous manner, as above, except that removal of a given aliquot of resin is not followed by performance of additional synthesis steps on the removed strand. To optimize hybridization properties it is ideal if the second population extends at least 6 bases beyond the 3' terminus of the Population 1 sequences. The simplest filler population for the family described above is depicted in Figure 7B (identified herein as SEQ ID NOs: 17-24). Note, that X's are used to indicate that the synthesis of a defined codon in each of these positions, most typically correspond to template or wild-type sequences, or a very limited variation of these. (FIG. 7B).

Please delete the paragraph beginning at page 37, line 3, with the following rewritten paragraph:

In a more complex synthesis regime, mutant recombination cassettes may be synthesized directly. For example, the oligonucleotides described with respect to Figure 6 are optionally synthesized mutagenically by synthesizing separately each of the 13 single codon mutagenized (NNC) oligos corresponding to each of the 40mers, excluding the last oligonucleotide which only partly encodes the sequence of interest. Briefly, synthesis is conducted in separately controlled flow cells for each of the desired sequences, resulting in approximately [(28 x 13) + (1 X 7)=] 91 distinct synthesis reactions, followed by the pooling of those sequences corresponding to

common recombination cassettes. See, Figure 8 (SEQ ID NOS 25-37). For example, oligonucleotides are optionally added in substantial molar excess over template (e.g., >1.5:1) to a mixture containing single stranded template (e.g., about 1 μg) corresponding to the opposite strand. The solution (e.g., 1x ligation buffer minus ATP) is heated to 99°C for 2 minutes, then cooled over 20 minutes to room temperature. Thereafter, ATP and T4 ligase are added to the mixture and the solution is incubated overnight, e.g., at about 13°C.

Please replace the previous Sequence Listing with the paper Sequence Listing attached hereto.

Additional Items

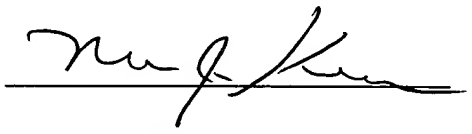
A Sequence Listing is provided herewith pursuant to 37 C.F.R. § 1.821. No new matter is introduced in the Sequence Listing, as the sequences in the Sequence Listing are identical to those in the Specification, Figure 7B and Figure 8. The Specification is being amended to reference the sequence identification numbers corresponding to those associated with the sequences in the Sequence Listing.

The sequence listing in Computer Readable Format accompanies this amendment. The undersigned hereby states that the paper copy of the Sequence Listing submitted concurrently herewith does not include matter which goes beyond the content of the application as filed, and that the Sequence Listing CRF enclosed is identical to the paper copy of the Sequence Listing.

No new matter is being introduced by entry of the foregoing amendments. Upon entry of these amendments, the application will be in compliance with the sequence rules of 37 CFR 1.821-1.825 and therefore qualified for examination under 35 U.S.C. §§ 131 and 132.

Respectfully submitted,

May 15, 2003



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